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Conference Abstract

# Exploring Options for Naming Taxa Based on DNA Sequences under the International Code of Nomenclature for Algae, Fungi, and Plants

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## Abstract

DNA sequence data has gained increasing importance in modern taxonomic research, and related subjects such as species identification, biogeography, evolution, and classification. Environmental DNA reveals numerous taxa that cannot be isolated or cultured using current techniques. Yet, the latest International Code of Nomenclature for algae, fungi, and plants requires physical specimens or illustrations as nomenclatural types for the formal naming of species and subspecific taxa (Turland et al. 2018). This limitation is impeding our ability to describe, study and communicate about a significant proportion of biodiversity.

Here we present the deliberations of a Special-purpose Committee established at the XIX International Botanical Congress in Shenzhen, China, to address the issue of DNA sequences as types. Two main options for resolving this problem were identified:

1. Amend the definition of a 'type' in the Code to include DNA sequences.
2. Allow the description of taxa without types under specific circumstances.

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Under either option, the Committee agreed to restrict the scope of the proposals to cases where the use of specimens or illustrations as types is not technically feasible (Thiele et al. 2023).

The inability to name taxa discovered through DNA sequencing has practical consequences that hinder research, conservation, and policy efforts. Whether this issue will be resolved depends on the voting at the Nomenclature Section of the XX International Botanical Congress to be held in Madrid in 2024. It is essential to engage with this process so that, whatever your opinion, your voice is heard at the Congress.

## Keywords

taxonomic classification, taxonomy, type specimens, typeless names

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## Conflicts of interest

The authors have declared that no competing interests exist.

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